

Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

Simpleaffy

RRID:SCR_001302

Type: Tool

Proper Citation

Simpleaffy (RRID:SCR_001302)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/simpleaffy.html>

Proper Citation: Simpleaffy (RRID:SCR_001302)

Description: Software package that provides high level functions for reading Affy .CEL files, phenotypic data, and then computing simple things with it, such as t-tests, fold changes and the like. It makes heavy use of the affy library. It also has some basic scatter plot functions and mechanisms for generating high resolution journal figures.

Abbreviations: Simpleaffy

Synonyms: Simpleaffy - Very simple high level analysis of Affymetrix data

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:16076888](#)

Keywords: affymetrix, annotation, data import, differential expression, microarray, one channel, preprocessing, quality control, report writing, transcription, visualization

Availability: GNU General Public License, v2 or newer

Resource Name: Simpleaffy

Resource ID: SCR_001302

Alternate IDs: OMICS_02034

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260912T195523+0000

Ratings and Alerts

No rating or validation information has been found for Simpleaffy.

No alerts have been found for Simpleaffy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 85 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#).

Gao YX, et al. (2025) Targeting LHPP in neoadjuvant chemotherapy resistance of gastric cancer: insights from single-cell and multi-omics data on tumor immune microenvironment and stemness characteristics. *Cell death & disease*, 16(1), 306.

Peng B, et al. (2024) Comprehensive landscape of m6A regulator-related gene patterns and tumor microenvironment infiltration characterization in gastric cancer. *Scientific reports*, 14(1), 16404.

He Y, et al. (2024) LINC00998 Modulating M2 Macrophage Activation in Allergic Rhinitis by Stabilizing BOB.1 mRNA. *Journal of inflammation research*, 17, 2309.

Chen B, et al. (2023) m6A and m5C modification of GPX4 facilitates anticancer immunity via STING activation. *Cell death & disease*, 14(12), 809.

Wang Q, et al. (2023) A compendium of mitochondrial molecular characteristics provides novel perspectives on the treatment of rheumatoid arthritis patients. *Journal of translational medicine*, 21(1), 561.

Alaskar A, et al. (2023) Inhibition of signaling downstream of beta-2 adrenoceptor by propranolol in prostate cancer cells. *The Prostate*, 83(3), 237.

Zhang B, et al. (2022) The chromatin remodeler CHD6 promotes colorectal cancer development by regulating TMEM65-mediated mitochondrial dynamics via EGF and Wnt signaling. *Cell discovery*, 8(1), 130.

Nie X, et al. (2022) N6-methyladenosine-related lncRNAs is a potential marker for predicting prognosis and immunotherapy in ovarian cancer. *Hereditas*, 159(1), 17.

Zhou J, et al. (2022) Pyroptosis patterns of colon cancer could aid to estimate prognosis, microenvironment and immunotherapy: evidence from multi-omics analysis. *Aging*, 14(18), 7547.

Li F, et al. (2021) m5C Regulator-Mediated Methylation Modification Patterns and Tumor Microenvironment Infiltration Characterization in Papillary Thyroid Carcinoma. *Frontiers in oncology*, 11, 729887.

Jiang Y, et al. (2021) Deciphering potential pharmacological mechanism of Sha-Shen-Mai-Dong decoction on primary Sjogren's syndrome. *BMC complementary medicine and therapies*, 21(1), 79.

Jin Y, et al. (2021) Analysis of Ferroptosis-Mediated Modification Patterns and Tumor Immune Microenvironment Characterization in Uveal Melanoma. *Frontiers in cell and developmental biology*, 9, 685120.

Marzec J, et al. (2021) The Transcriptomic Landscape of Prostate Cancer Development and Progression: An Integrative Analysis. *Cancers*, 13(2).

G??zen D, et al. (2021) Transcriptome profiles associated with selenium-deficiency-dependent oxidative stress identify potential diagnostic and therapeutic targets in liver cancer cells. *Turkish journal of biology = Turk biyoloji dergisi*, 45(2), 149.

Zhang W, et al. (2021) Molecular subtypes based on ferroptosis-related genes and tumor microenvironment infiltration characterization in lung adenocarcinoma. *Oncoimmunology*, 10(1), 1959977.

Dom G, et al. (2021) Transcriptomic Signature of Human Embryonic Thyroid Reveals Transition From Differentiation to Functional Maturation. *Frontiers in cell and developmental biology*, 9, 669354.

Jin Y, et al. (2021) Analysis of m6A-Related Signatures in the Tumor Immune Microenvironment and Identification of Clinical Prognostic Regulators in Adrenocortical Carcinoma. *Frontiers in immunology*, 12, 637933.

Zhang B, et al. (2020) m6A regulator-mediated methylation modification patterns and tumor microenvironment infiltration characterization in gastric cancer. *Molecular cancer*, 19(1), 53.

Liu D, et al. (2020) Association of an anaplastic lymphoma kinase pathway signature with cell de-differentiation, neoadjuvant chemotherapy response, and recurrence risk in breast cancer. *Cancer communications (London, England)*, 40(9), 422.

Bil P, et al. (2020) Circuits Regulating Superoxide and Nitric Oxide Production and Neutralization in Different Cell Types: Expression of Participating Genes and Changes Induced by Ionizing Radiation. *Antioxidants (Basel, Switzerland)*, 9(8).